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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	71.06 Secon gnments)	Title: US-09-665-363-6 Perfect score: 1658 Sequence: 1 ctagtacgcctgtggaacgcgcagagagacaagataag 1658 Scoring table: IDENTITY_NUC		: Minimu Maximu Listin	11.*  11.*

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Submitted (18-AUG-1998) to the DDBJ/EMBL/GenBank databases. Aki Horli, Tohoku University School of Medicine, Department of Molecular Pathology; 2-1 Seiryo-machi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mall.cc.tohoku.ac.ip, Tel:81-22-717-8047)
Location/Qualifiers
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Direct Submission

Direct Submission

Submitted (18-Aug-1998) to the DDBJ/EMBL/GenBank databases. Akira

Horii, Tohoku University School of Medicine, Department of

Molecular Pathology, 2-1 Sairyo-machi, Aoba-ku, Sendai, Miyagi

980-8775, Japan (E-mail:horii@mail.cc tohoku.ac.jp,

Tel:81-22-717-8042, Fax:81-22-717-8047)

Location/Qualifiers

1. 987

/db_arref="taxon:9606"

233. 551
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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The human PMSL proteins do not interact with hMLH1, a major mismatch repair protein
1. Blochem. 125 (4), 818-825 (1999)
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Horii,A.
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1 O81785 arabidopsis thaliana
1 Oftro deinococcus radiodura
1 Q9he21 neurospora crassa.re
1 Q12083 saccharomyces cerevis
1 O9h1a8 homo sapiens (human).
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MEDLINE-99203588; Pubmed-10104297;
Kondo E., Horil A., Fukushige S.;
"The human PMS2L proteins do not interact with hMLH1, a major DNA
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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InterPro; IPR002099; DNA_mis_repair.
Pfam; PF01119; DNA_mis_repair; 1.
SEQUENCE 297 AA; 32669 MW; 9D05D86F583B917D CRC64;
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7-Riochem. 125:818-825(1999)....

EMBL; AB017005; BAA74754.1; -.
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US-09-665-363-6 x 095744
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13 664 109v380 drosophila melanogaste

727 109c5f9 arabidopsis thaliana (mc

737 109czv4 arabidopsis thaliana (mc

633 109hul8 pseudomonas aeruginosa.

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12 887 109bix4 trypanosoma brucei. ml

637 109bax4 trypanosoma brucei. ml
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                                                                                                           About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
        out_format : pfs
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219.00 336.35 2.9e-11
        OM of: US-09-665-363-6 to: SPTREMBL_17:*
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Query, 08.09 665-363 6
Query length: 1658
Database: SPTREMBL_17:*
Database sequences: 473505
Database length: 146272329
Search time (sec): 142.870000
                                                        Date: Mar 12, 2002 11:08 PM
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sp_bacteria:Q9KAC1 + 2:
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sp_bacteria:099XN7
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sp_plant:09ZRV4
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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"The sequence of Homo sapiens PAC clone DJ0953A04.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
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986 GATGTGGGGTAGAAGAAGAAACTTCGAAGGCTTATCTCTTTCAGCTCTG
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01-NOV-1999 (TrEMBLrel. 12, Last seque)
01-JUN-2001 (TrEMBLrel. 17, Last annoti
WUGSC:H_DJU953A04.2 PROTEIN (FRAGMENT)
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rn 09Y2N0 PRELIMINARY;
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Submitted (NOV-1998)
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GCCGTGATTGTCAGTTTCTTGAGGCTCCCCAGCCATGCTTCCTGTACAG 1395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.;
Submitted (Apr-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (Apr-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (Apr-1999) to the EMBL/GenBank/DDBJ databases.
HSSP: P23367; 1BKN.
HSSP: P23367; 1BKN.
HSSP: P23367; 1BKN.
HSSP: PF01119; DNA_mis_repair.
NON_TER.
                                                                                                                                                                                                                                                                                              796 ACAGAACCIGCIAAGGCCATCAAACCIATIGAICGGAAGICAGICCATCA
                                                                                                                                                                                                                                                                                                                                                       846 GATTTGCTCTGGGCCGGTGGTACTGAGTCTAAGCACTGCGGTGAAGAAGA
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                                                                                                254 AA; 27442 MW; 923FE4A3002BBFC3 CRC64;
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Gaps: 1
Percent Identity: 96.585
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Quality: 1024.50
Ratio: 5.072
Retrio: 98.537
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US-09-665-363-6 x Q9Y2N0
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